REMARKS

Enclosed herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a substitute Sequence Listing to be inserted into the specification as indicated above. The substitute Sequence Listing in no way introduces new matter into the specification.

Also submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the substitute Sequence Listing. The disk copy of the substitute Sequence Listing, file "3631-0107P.ST25", is identical to the paper copy, except that it lacks formatting.

The substitute Sequence Listing includes sequences disclosed in the Specification as filed that were not made part of the original Sequence Listing. The amendments to the Specification are being made to reference the sequences found in the Specification by their SEQ ID NOS. These amendments are editorial in nature and do not constitute new matter.

Entry of the above amendments is earnestly solicited. An early and favorable first action on the merits is earnestly solicited.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

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LRS/KW
3631-0107P

Attachments: Paper and disk copy of Sequence Listing
Copy of Notice to Comply
Copy of Version with Markings to Show Changes Made

VERSION WITH MARKINGS TO SHOW CHANGES MADE

The paragraph beginning on page 37, line 10 has been amended as follows:

One especially preferred PADRE peptide is the one having the amino acid sequence AKFVAAWTLKAAA (SEQ ID NO:19) or an immunologically effective subsequence thereof. This, and other eptiopes having the same lack of MHC restriction are preferred T-cell epitopes which should be present in the analogues used in the inventive method. Such super-promiscuous epitopes will allow for the most simple embodiments of the invention wherein only one single modified amyloidogenic polypeptide is presented to the vaccinated animal's immune system.

The paragraph beginning on page 58, line 6 has been amended as follows:

It should be noted that preferred modified amyloidogenic molecules comprises modifications which results in a polypeptide having a sequence identity of at least 70% with an amyloidogenic protein or with a subsequence thereof of at least 10 amino acids in length. Higher sequence identities are preferred, e.g. at least 75% or even at least 80, 85, 90 or 95%. The sequence identity for proteins and nucleic acids can be calculated as $(N_{ref} - N_{dif}) \cdot 100/N_{ref}$, wherein N_{dif} is the total number of non-identical residues in the two sequences when aligned and N_{ref} is the number of residues in one of the sequences. Hence, the DNA sequence AGTCAGTC (SEQ ID NO:17) will have a sequence identity of 75% with the sequence AATCAATC (SEQ ID NO:18) (N_{dif}=2 and N_{ref}=8).